

GenCore version 5.1.6
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES									
Result No.	Score	Query Match	Length	DB ID	Description				
1	2725	100.0	2725	6 AX355102	AX355102 Sequence				
2	2725	100.0	2725	9 HSDBIRRA	X13255 Human mRNA				
3	2717	99.7	2807	9 BC017174	Homo sapi				
4	2425	89.0	2425	9 HSDBIRB	X13256 Human mRNA				
5	1940	71.2	1955	9 HSDBH	Y00996 Human mRNA				
6	1805.2	66.2	1812	12 BT007470	Synthetic				
7	1702.8	62.5	3842	4 AB029430	EQUUS CAB				
8	1498	55.0	2317	4 AF118638	BOS TAURI				
9	1476.8	54.2	2322	4 BOVADBM	J02890 Bovine adre				
10	1419.2	52.1	1840	4 BOVDDBH	J05160 Bovine dopa				
11	1412.8	51.8	2195	4 BOVDBHZ	J02809 Bovine dopa				
12	1236.8	45.4	2274	10 SS0200	MUS MUSCULUS				
13	1219.4	44.7	2443	10 RATDOPHY	L12407 Rattus norv				
14	1016.8	37.3	1092	9 HSDBH12	X13268 Human DNA F				
C	15	1016.8	37.3	46651	AC000404 Genomic S				
C	16	1016.8	37.3	53242	9 AL365494 Human DNA				
C	17	1016.8	37.3	110000	2 AL954350_3				
C	18	1001.2	36.7	110000	2 AL954350_0				
C	19	330	12.1	2037	9 HSDBH1				
C	20	328.4	12.1	37584	9 AC001227				
C	21	326.6	12.0	505	5 GGA51457				
C	22	258.4	9.5	276	9 HSDBH3				
C	23	239.6	8.8	262	9 AF070919				
C	24	228.4	8.4	2894	3 DMTBHMR				
C	25	228.4	8.4	73066	10 AL954801				
C	26	228.4	8.4	186208	2 AC010965				
C	27	228.4	8.4	205420	2 AC091762				
C	28	221.6	8.1	663	5 AF075385				
C	29	220	8.1	225079	2 AC126203				
C	30	193	7.1	2037	6 AX347199				
C	31	193	7.1	2037	6 AX348532				
C	32	180	6.6	195	9 HSDBH4				
C	33	179.6	6.6	2037	6 AX347198				
C	34	179.6	6.6	2037	6 AX348531				
C	35	175.8	6.5	2164	10 BC037684				
C	36	174.2	6.4	2903	10 AB041606				
C	37	172	6.3	2796	10 BC025892				
C	38	170	6.2	185	9 HSDBH2				
C	39	166.8	6.1	2906	9 AF12963				
C	40	163.8	6.0	178	9 HSDBH1				
C	41	151.4	5.6	2188	9 BC018756				
C	42	149.2	5.5	162	9 HSDBH7				
C	43	149	5.5	165	9 HSDBH2				
C	44	146.8	5.4	2150	6 AX44056				
C	45	146.8	5.4	2988	6 AX195189				
C	46	141.8	5.2	2762	6 BD127343				
C	47	141.8	5.2	2762	2 AC013218				
C	48	141.8	5.2	2960	9 AK074879				
C	49	140.6	5.2	2939	9 AV007239				
C	50	138.4	5.1	2184	6 AR243796				
C	51	134.8	4.9	2312	5 AF32750				
C	52	131	4.8	146	9 HSDBH1				
C	53	113	4.1	40265	2 AC013218				
C	54	113	4.1	181178	3 AC023713				
C	55	113	4.1	315362	3 AE003442				
C	56	106	3.9	2139	9 HSDBH5				
C	57	105	3.9	2139	9 AF12964				
C	58	101.8	3.7	1860	10 AB065134				
C	59	101	3.7	129616	2 AL95290				
C	60	94.6	3.5	155030	2 AC141807				
C	61	90.2	3.3	29355	3 CEH3N06				
C	62	88.8	3.3	2122	9 HSMB00558				
C	63	77.2	2.8	125020	9 AF449315				
C	64	74.4	2.7	140320	2 DMBS11F15				
C	65	65.8	2.4	2726	3 AY071594				

Pred. No. is the number of results predicted by chance to have a

Potash, J. Association of dopamine beta-hydroxylase polymorphisms with bipolar disorder									
PATENT : WO 018600-A 1 15-NOV-2001; WHITEHORN INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; THE GENERAL HOSPITAL CORPORATION (US) ; JOHNS HOPKINS UNIVERSITY (US)									
TITLE		JOURNAL							
AC014422 Drosophil		WHITEHORN INSTITUTE FOR BIOMEDICAL RESEARCH (US) ; THE GENERAL HOSPITAL CORPORATION (US) ; JOHNS HOPKINS UNIVERSITY (US)							
AC010066 Drosophil		HUMAN GENOME PROJECT							
AC003528 Drosophil		HUMAN GENOME PROJECT							
X14357 Human DNA f		HUMAN GENOME PROJECT							
AY098944 Homarus a		HUMAN GENOME PROJECT							
AF429315 Homo sapi		HUMAN GENOME PROJECT							
AF323239 Bordetella		HUMAN GENOME PROJECT							
AY207049 Homo sapi		HUMAN GENOME PROJECT							
AX655393 Sequence		HUMAN GENOME PROJECT							
AX655393 Sequence		HUMAN GENOME PROJECT							
AF232941 Bordetella		HUMAN GENOME PROJECT							
1130342 Bordetella		HUMAN GENOME PROJECT							
AL939125 Streptomy		HUMAN GENOME PROJECT							
X15867 Microboccus		HUMAN GENOME PROJECT							
AY128334 Mycobacte		HUMAN GENOME PROJECT							
AF232940 Bordetell		HUMAN GENOME PROJECT							
AC079433 Mus muscu		HUMAN GENOME PROJECT							
AX527902 Sequence		HUMAN GENOME PROJECT							
AX527904 Sequence		HUMAN GENOME PROJECT							
AX07613 Sequence		HUMAN GENOME PROJECT							
BC000040 Homo sapi		HUMAN GENOME PROJECT							
BC001648 Homo sapi		HUMAN GENOME PROJECT							
AP005829 Oryza sat		HUMAN GENOME PROJECT							
D83327 Rice (YK426		HUMAN GENOME PROJECT							
AP005048 Streptomy		HUMAN GENOME PROJECT							
AE00563 Haloacte		HUMAN GENOME PROJECT							
AP005044 Streptomy		HUMAN GENOME PROJECT							
AB010951 Streptomy		HUMAN GENOME PROJECT							
AP005035 Streptomy		HUMAN GENOME PROJECT							
AP003872 Oryza sat		HUMAN GENOME PROJECT							
AP004636 Oryza sat		HUMAN GENOME PROJECT							
AC108756 Oryza sat		HUMAN GENOME PROJECT							
BD14963 Primer fo		HUMAN GENOME PROJECT							
BD126373 Primer fo		HUMAN GENOME PROJECT							
AL37093 Human chr		HUMAN GENOME PROJECT							
AP005024 Streptomy		HUMAN GENOME PROJECT							
AP004632 Azorobact		HUMAN GENOME PROJECT							
AP002962 Homo sapi		HUMAN GENOME PROJECT							
Continuation (22 o		HUMAN GENOME PROJECT							
AB088224 Streptomy		HUMAN GENOME PROJECT							
AC136100 Rattus no		HUMAN GENOME PROJECT							
AL71305 Oryza sat		HUMAN GENOME PROJECT							
AL731887 Oryza sat		HUMAN GENOME PROJECT							
AL64068 Ralstonia		HUMAN GENOME PROJECT							
AL939128 Streptomy		HUMAN GENOME PROJECT							
BD179703 Highly th		HUMAN GENOME PROJECT							
AC136100 Macaca fa		HUMAN GENOME PROJECT							
BD179535 Highly th		HUMAN GENOME PROJECT							
MB1835 Human alpba		HUMAN GENOME PROJECT							
AB011711 Xanthomon		HUMAN GENOME PROJECT							
Contiuination (12 o		HUMAN GENOME PROJECT							
AX211706 Sequence		HUMAN GENOME PROJECT							
AC068645 Homo sapi		HUMAN GENOME PROJECT							
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421 CCCTGGTTTCAGAGGCCCTTGGGACTCGGACCCAGGATTACTTGAAGACCG		HUMAN GENOME PROJECT							
481 GCACGTCCACTTGGGACTCGGACCCAGGATTACTTGAAGACCG		HUMAN GENOME PROJECT							
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ALIGNMENTS			
RESULT 1			
LOCUS	X356102	Sequence 1 from Patent WO0186000.	PAT 06 - FEB-2002
DEFINITION	AX356102	2725 bp	DNA
ACCESSION	AX356102	linear	
KEYWORDS	GT:18620653		
ORGANISM	Homo sapiens (human)		
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE 1	QY	601 AACCGGAGTGGCTCAGAGCGTGCACCATGGAGTCCAAAGCTCCATATCCAGATCC	660
AUTHORS Sklar, P., Lander, E.S., McInnis, M.G., Depaulo, J.R., Willour, V. and	Db	601 AACCGGAGTGGCTCAGAGCGTGCACCATGGAGTCCAAAGCTCCATATCCAGATCC	660
	QY	661 CCAGCGAGGAGACCACGTACTGGTCTACATTAGGAGTTCCAAGGGCTTCCTCGGC	720
	Db	661 CCAGCGAGGAGACCACGTACTGGTCTACATTAGGAGTTCCAAGGGCTTCCTCGGC	720
	QY	721 ACCACATTACAAGTAGGCCCATGTCACCAAGGGCATAGGCCCCTGTCCACACA	780
	Db	721 ACCACATTACAAGTAGGCCCATGTCACCAAGGGCATAGGCCCCTGTCCACACA	780
	QY	781 TGGAGTCTCCATGTGGCCCCAGATGGCACGGTCCCCACTTGCGGCCCTGG	840
	Db	781 TGGAGTCTCCATGTGGCCCCAGATGGCACGGTCCCCACTTGCGGCCCTGG	840

JOURNAL	Nucleic Acids Res.	17 (3), 1089-1102 (1989)	Qy	421 CCCCTGTTTCAGGGCCCTTGGCACTTGACCCCCAAGGATTACCTCATGGAGCAGC 480
PUBMED	89160241		Db	421 CCCCTGTTTCAGGGCCCTTGGCACTTGACCCCCAAGGATTACCTCATGGAGCAGC 480
REFERENCE	2 (bases 1 to 2725)			
AUTHORS	Nagatsu,T.			
TITLE	Direct Submission			
JOURNAL	Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan		Qy	481 GCACTGTCCACTTGTCACTGGATCTCGGATCTGGAGGGCGCTTCCGGTCACTGGGGCATCA 540
COMMENT	see also X13256 for type b mRNA from Craig et al. Cyogenet. Cell Genet. 48:48-50 (1988).		Db	481 GCACTGTCCACTTGTCACTGGATCTCGGATCTGGAGGGCGCTTCCGGTCACTGGGGCATCA 540
FEATURES	Map data from Craig et al. Cyogenet. Cell Genet. 48:48-50 (1988).		Qy	541 ACGGGAACTTGCCTTCAAGCCTGACCATGGGTCAGCTGGAGGGTGTCAAGCTGGGGCATCA 600
source	Location/Qualifiers		Db	541 ACGGGAACTTGCCTTCAAGCCTGACCATGGGTCAGCTGGAGGGTGTCAAGCTGGGGCATCA 600
	1. .2725			
	/organism="Homo sapiens"			
	/mol_type="mRNA"			
CDS	/db_xref="taxon: 9606"		Qy	601 AACGGGAACTTGCCTTCAAGCCTGACCATGGGTCAGCTGGGGCATCAAGCTGGGGCATCA 660
	/map_xref="9q34"		Db	601 AACGGGAACTTGCCTTCAAGCCTGACCATGGGTCAGCTGGGGCATCAAGCTGGGGCATCA 660
	33 . 1844			
	/codon_start=1		Qy	661 CCACCCAGAGACCCTGACTGTGTCAATTAAGGAGCTTCCAAGGGTGTCTCGGCC 720
	/product="dopamine beta-hydroxylase preprotein (AA -25 to 578)"		Db	661 CCACCCAGAGACCCTGACTGTGTCAATTAAGGAGCTTCCAAGGGTGTCTCGGCC 720
	/protein_id="CAA31631.1"			
	/db_xref="IGI: 30474"		Qy	721 ACCACATAATCAGTAAAGGCCATCTTCAAGGGCAATAGGGCCATTCAGGAACTTCCACACA 780
	/db_xref="SWISS-PROT: P09172"		Db	721 ACCACATAATCAGTAAAGGCCATCTTCAAGGGCCATTCAGGAACTTCCACACA 780
	/translation="MREAFMFYSPAVAFPLVILVAALOGSAPRESPLPYHTPLDPEGS		Qy	781 TGGAAAGTCTTCCAGTGGCCCCGAGATGGACAGCTGTCGGGGCCCTGGCG 840
	SDOKGQTHIDPDDQYDQOQYRFLKAGVLFGMSRGELENADLVILWDTGDTTYFADAW		Db	781 TGGAAAGTCTTCCAGTGGCCCCGAGATGGACAGCTGTCGGGGCCCTGGCG 840
	EPFRSELEAINGSLGLORLKPNTPELPFLPSDACTMEYPAFNPOIIPSEETTYWC			
	RLLNCRHVLAAWALGAKARYTPEBACFLVRLRFLPQYRFLPQYRFLPQYRFLPQYRFL		Qy	841 ACTCCAAAGTAGAAACCGACGCCCTGAACATCTGGCCACCTGGCTGGCC 900
	YKEPLPKGFRRHITKYPEPFLVTKRUVTVLVRDGEWEITVNQHYSPIFOEITMLKKVVVSHPGDVLI		Db	841 ACTCCAAAGTAGAAACCGACGCCCTGAACATCTGGCCACCTGGCTGGCC 900
	SCNTYNTDEBLATGGFELMEVNYHYPPOTOLELKCTTFLKQYFLHNLRF			
	NNEDEVTCQPQASISQQFTSPVPMWSNRDVLYKALYSFAP1SMICNSAARFQENLQ		Qy	901 TGGGTGCAAGSGCATATCTCCCTGAAAGTICAATACCAAGAACCACTGTGATAAGCGAA 960
	PLPKVTPVTEPTPQCPISQGRSPAGPTVSTCGKGK"		Db	901 TGGGTGCAAGSGCATATCTCCCTGAAAGTICAATACCAAGAACCACTGTGATAAGCGAA 960
sig_peptide	33 . 107			
mat_peptide	/note="signal peptide (AA -25 to -1)"		Qy	961 CTCCTCGAGATATCTCCCTGAAAGTICAATACCAAGAACCACTGTGATAAGCGAA 1020
BASE COUNT	533 a 901 c 774 g 517 t		Db	961 CTCCTCGAGATATCTCCCTGAAAGTICAATACCAAGAACCACTGTGATAAGCGAA 1020
ORIGIN				
Query Match	100.0%	Score 2725; DB 9; Length 2725;	Qy	1021 AGACTCTCAGGATCCGGTCACTACAGGAACTGGGGCTTCACCGGAGGGGGAA 1080
Best Local Similarity	100.0%	Pred. No. 0; Mismatches 0; Indels 0; Gaps 0;	Db	1021 AGACTCTCAGGATCCGGTCACTACAGGAACTGGGGCTTCACCGGAGGGGGAA 1080
Matches 2725;	Conservative			
Qy	1 TCAGCTGGCTGGCCAGCCCTGCCCTGCCAGCATGGGAGGGAGCTCATGGCA 60		Qy	1081 TCATGGAGCTGGACTGGCTACAGGCCAGTGGCTGGCACTGGCACTGGGGCT 1140
Db	1 TCAGCTGGCTGGCCAGCCCTGCCCTGCCAGCATGGGAGGGAGCTCATGGCA 60		Db	1081 TCATGGAGCTGGACTGGCTACAGGCCAGTGGCACTGGCACTGGGGCT 1140
Qy	61 CAGCAGTGGCATCTTCGGTCACTCCGGTCACTGGGGCTGGCTCCCGTGTG 120		Qy	1141 TCATCTCTCACTGGCTACAGGCCAGTGGCACTGGCACTGGGGCT 1200
Db	61 CAGCAGTGGCATCTTCGGTCACTCCGGTCACTGGGGCTGGCTCCCGTGTG 120		Db	1141 TCATCTCTCACTGGCTACAGGCCAGTGGCACTGGGGCT 1200
Qy	121 AGAGCCCTCCCTCATCACATCCCCTGGTCACTCCGGTCACTGGGGCTGGCT 180		Qy	1201 TCCACATCTCTGGCTTCACAGGCCAGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1260
Db	121 AGAGCCCTCCCTCCCTATCACATCCCCTGGTCACTGGGGCTGGCT 180		Db	1201 TCCACATCTCTGGCTTCACAGGCCAGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1260
Qy	181 ATGTCAGTACACCCAGGGCCATCCATTTCCAGCTCTGGTGGGGCTGGCT 240		Qy	1261 TGGTGGGAGATGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1320
Db	181 ATGTCAGTACACCCAGGGCCATCCATTTCCAGCTCTGGTGGGGCTGGCT 240		Db	1261 TGGTGGGAGATGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1320
Qy	241 GCGTCCTGTTGGGATGTCGGACGCTGGCAGCTGGGCTGGCTCATGGCT 300		Qy	1321 TCCAGGAGATTCGGCATGGTGGGGAGATGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1380
Db	241 GCGTCCTGTTGGGATGTCGGACGCTGGCAGCTGGCTGGCTCATGGCT 300		Db	1321 TCCAGGAGATTCGGCATGGTGGGGAGATGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1380
Qy	301 GGACCGATGGGCAACTCTCTTGGGATGTCGGACGCTGGCAGCTGGCTCATGGCT 360		Qy	1381 CCTCCCTGGCAGCTGGGAGACCGGGAGCTGGGGCTTCGGGATCACTGGGGCT 1440
Db	301 GGACCGATGGGCAACTCTCTTGGGATGTCGGACGCTGGCTCATGGCT 360		Db	1381 CCTCCCTGGCAGCTGGGAGACCGGGAGCTGGGGCTTCGGGATCACTGGGGCT 1440
Qy	361 ACCTGGATCCCCAGGAGACTACAGCTGGCTGGGAGGGACCCAGAAAGGCCCTGA 420		Qy	1441 TGAGGAGATGTGGGGAGATGTGGGGAGATGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1500
Db	361 ACCTGGATCCCCAGGAGACTACAGCTGGCTGGGAGGGACCCAGAAAGGCCCTGA 420		Db	1441 TGAGGAGATGTGGGGAGATGTGGGGAGATGTGGGGAGATGTGAAACCACTCATCATGGGGCT 1500
Qy			Qy	1501 AGACGGCTGTGGACGGCCGGCTTCCTGAGAAGTACTCCACCTCATACAGGTCAACA 1560

BASE COUNT	589	a	909	c	788	g	521	t
ORIGIN								
Query Match	99.7%		Score 2717;	DB 9;	Length 2807;			
Best Local Similarity	99.8%		Pred. No. 0;					
Matches 2720;	Conservative 0;	Mismatches	5;	Indels 0;	Gaps 0;			
Qy	1	TCAGTCGTGGCCAGCTGGGCCAGCATGGGAGGCCAGCATGCTGAGCTTACATGCTAGCA	60					
Db	15	TCACTCTGGCCAGCTGGGCCAGATGGGAGGCCAGCATGCTGAGCTTACATGCTAGCA	74					
Qy	61	CAGCACTGGCCATCTCTGGCTCATCTGTGGCCACTGGGGCTGGCTCCCGTG	120					
Db	75	CAGCACTGGCCATCTCTGGCTCATCTGTGGCCACTGGGGCTGGCTCCCGTG	134					
Qy	121	AGAGCCCCCTCCCTATCACATCCCCCTGGGCCAGCCGAGGGTCTGGCTCATGGGA	180					
Db	135	AGAGCCCCCTCCCTATCACATCCCCCTGGGCCAGCCGAGGGTCTGGCTCATGGGA	194					
Qy	181	ATGTCGCTATAACCCGGAGCCAATCATTCAGCTCCTGGGGAGGCTCAAGGCTG	240					
Db	195	ATGTCGCTATAACCCGGAGCCAATCATTCAGCTCCTGGGGAGGCTCAAGGCTG	254					
Qy	241	GCGTCCTGTTGGATGCCACCTGGGATCTGGGAGCTGAGAACATCTGTGGCTCT	300					
Db	255	GCGTCCTGTTGGATGCCACCTGGGATCTGGGAGCTGAGAACATCTGTGGCTCT	314					
Qy	301	GGACCGATGGGACATCTGGCTATTGGGAGCCCTGGAGTGCACAGAAGGGCAGATCC	360					
Db	315	GGACCGATGGGACATCTGGCTATTGGGAGCCCTGGAGTGCACAGAAGGGCAGATCC	374					
Qy	361	ACCTGGATCCCAGGAGGACTACCAGCTGGAGGGACCCAGAACGGCTCTA	420					
Db	375	ACCTGGATCCCAGGAGGACTACCAGCTGGAGGGACCCAGAACGGCTCTA	434					
Qy	421	CCCTGCTTTTCAAGAGGCCCTTGGACCTGGGACCCAGGATTACCTCTTAAAGAGC	480					
Db	435	CCCTGCTTTCAAGAGGCCCTTGGACCTGGGACCCAGGATTACCTCTTAAAGAGC	494					
Qy	481	GCACTGTCACCTGGTACGGATCTGGGCTGAGGGCTGAGCTCCGTCATGGGCCATCA	540					
Db	495	GCACTGTCACCTGGTACGGATCTGGGCTGAGGGCTGAGCTCCGTCATGGGCCATCA	554					
Qy	541	ACGCTCGGCCCTCGAATGGGCTGCACTGGGCTTGGACCTGGGACCTGGGCTG	600					
Db	555	ACGCTCGGCCCTCGAATGGGCTGCACTGGGCTGAGGGCTGAGCTCCGTCATGGGCCATCA	614					
Qy	601	AACCGGAGAGGACCCACTGCTGGCTCAAGCGCTGACCATGGGCTCAAGTCCCAATATCCGTC	660					
Db	615	AACCGGAGAGGACCCACTGCTGGCTCAAGCGCTGACCATGGGCTCAAGTCCCAATATCCGTC	674					
Qy	661	CCAGCCAGGAGGACCCACTGCTGGCTCAAGCGCTGACCATGGGCTCAAGTCCCAATATCCGTC	720					
Db	675	CCAGCCAGGAGGACCCACTGCTGGCTCAAGCGCTGACCATGGGCTCAAGTCCCAATATCCGTC	734					
Qy	721	ACCACATATCAAGTAGGAGGCCATCTCAAGGGCAATGGGCCCTGAGGGCTG	780					
Db	735	ACCACATATCAAGTAGGAGGCCATCTCAAGGGCAATGGGCCCTGAGGGCTG	794					
Qy	781	TGGAAGCTTCCAGTGCCCGAGATGGACGGGCCCACTTGAGGGCTTCAAGGGCAATGGGCCCTGCG	840					
Db	795	TGGAAGCTTCCAGTGCCCGAGATGGACGGGCCCACTTGAGGGCTTCAAGGGCAATGGGCCCTGCG	854					

Qy	841	ACTCCAAAGATGAAACCAGGCCCTCAACTACTGCCGACCGTGTGGCGCCTGGGCC	900
Db	855	ACTCCAAAGATGAAACCAGGCCCTCAACTACTGCCGACCGTGTGGCGCCTGGGCC	914
Qy	901	TGGGTGCCAAGGGATTTTTACTACCCAGGAAACCGGCCCTGGCTTGCGTTGGGGTCAGGGT	960
Db	915	TGGGTGCCAAGGGATTTTTACTACCCAGGAAACCGGCCCTGGCTTGCGTTGGGGTCAGGGT	974
Qy	961	CCTCCAGATACTCGCCTGGAAAGTTCACTACCAACCAACTGGTATAGAACGAGAA	1020
Db	975	CCTCCAGATACTCGCCTGGAAAGTTCACTACCAACCAACTGGTATAGAACGAGAA	1034
Qy	1021	ACCACTCTAGCCTAGCCTGCTTACTACACCCAAACCTGCGGCTTCAAGCGGGGA	1080
Db	1035	ACCACTCTAGCCTAGCCTGCTTACTACACCCAAACCTGCGGCTTCAAGCGGGGA	1094
Qy	1081	TCATGGAGCTGGACATCGCTACCGCAGTAATGGCTTACAGCCAACTGGGACCGCT	1140
Db	1095	TCATGGCTGGACATGGCTACCGCAGTAATGGGACCTCCCTCCGGGA	1154
Qy	1141	TCATCCCTACATGGCTACCGCAGGA2AGTGCACCCGCTGCACACTCCCTCCGGGA	1200
Db	1155	TCATCCCTACATGGCTACCGCAGGA2AGTGCACCCGCTGCACACTCCCTCCGGGA	1214
Qy	1201	TCCACATCTTGCCTCTAGCTCACACACACCTGAACTGGGAAACCTGGGTACAGTGC	1260
Db	1215	TCCACATCTTGCCTCTAGCTCACACACACCTGAACTGGGAAACCTGGGTACAGTGC	1274
Qy	1261	TGGTGGGGACGGCGGGAGTGGGAGATCGTGAACAGGAGAACGGACAATCACTA	1320
Db	1275	TGGTGGGGACGGCGGGAGTGGGAGATCGTGAACAGGAGAACGGACAATCACTA	1334
Qy	1321	TCCAGGAAATCCGATGTTGAAAGGTGCTGTTCACTACCCAGGAGCTCTACT	1380
Db	1335	TCCAGGAAATCCGATGTTGAAAGGTGCTGTTCACTACCCAGGAGCTCTACT	1394
Qy	1381	CCTCCCTGACGGTACACACCGGAAGACCGGAGCTGGCAACAGTGGGGGATCTCA	1440
Db	1395	CCTCCCTGACGGTACACACCGGAAGACCGGAGCTGGCAACAGTGGGGGATCTCA	1454
Qy	1441	TGGAGGAGATGTTGCAACTACATGTCACACTACTACCCAGGAGCTGAGCTCTGCA	1500
Db	1455	TGGAGGAGATGTTGCAACTACATGTCACACTACTACCCAGGAGCTGAGCTCTGCA	1514
Qy	1501	AGACGGCTGTGAGCCGGTTCTGCAAGAGTACTTCCACCTCATCACAGGTTCAACA	1560
Db	1515	AGACGGCTGTGAGCCGGTTCTGCAAGAGTACTTCCACCTCATCACAGGTTCAACA	1574
Qy	1561	ACGGGATCTCTGACCTCCCTAGGGCTCCNGTCTAGCAGTTCACTCTGTTCCCT	1620
Db	1575	ACGGGATCTCTGACCTCCCTAGGGCTCCNGTCTAGCAGTTCACTCTGTTCCCT	1634
Qy	1621	GGAACCTCTCAACGGCAGCTACTGAGGGCCCTGTATGGCTTGGCCCATTCATRG	1680
Db	1635	GGAACCTCTCAACGGCAGCTACTGAGGGCCCTGTATGGCTTGGCCCATTCATC	1694
Qy	1681	ACTGCAAAAGATGCTCAACCCGACGACTGAAAGCTGGTATGGAAACCTGGCC	1740
Db	1695	ACTGCAAAAGATGCTCAACCCGACGACTGAAAGCTGGTATGGAAACCTGGCC	1754
Qy	1741	AGGTCACTCCACACTGGAAAGCCCCACAGTGCCCCACAGGGCTGAGGGGACCTACTCCT	1800
Db	1755	AGGTCACTCCACACTGGAAAGCCCCACAGGGCTGCCCCACAGGGCTGAGGGGACCTACTCCT	1814
Qy	1801	CTGCTGGCCCAACCGTGTGTCAGCATGGGGCAAAAGCTGAGGGGACCTACTCCT	1860
Db	1815	CTGCTGGCCCAACCGTGTGTCAGCATGGGGCAAAAGCTGAGGGGACCTACTCCT	1874
Qy	1861	CCCCCTCTCCATGCTGCTCCCTGTTGGCTCAACCGGCACTGTGCACTCTA	1920
Db	1875	CCCCCTCTCCATGCTGCTCCCTGTTGGCTCAACCGGCACTGTGCACTCTA	1934
Qy	1921	GATCCCCATGAAACAGCCCTGACGCCAGGATGAGGGGCAAGCCCTGAGCTG	1980

Human Dopamine Beta-Hydroxylase Preprotein (AA 1-578)									
Accession	Organism	Protein ID	Peptide ID	Peptide Sequence	Peptide Length	Peptide Score	Peptide Match Type	Peptide Match Score	Peptide Match Description
NP_00160241	Homo sapiens	CAA1632.1	1	MEDLINE	89160241	89.0%	Query Match	89.0%	Score 2425; DB 9; Length 2425;
PUBMED			2	PUBMED	2922261	100.0%	Best Local Similarity	100.0%	Pred. No. 0; Missmatches 0; Indels 0; Gaps 0;
REFERENCE			3	REFERENCE	(bases 1 to 2425)				
AUTHORS	Nagatsu,T.		4	AUTHORS	Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan				
TITLE	Direct Submission		5	TITLE	Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan				
JOURNAL			6	JOURNAL	Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988). Location/Qualifiers				
COMMENT			7	COMMENT					
FEATURES			8	FEATURES					
SOURCE			9	SOURCE					
			10						
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Db	421	CCCTGCTTTCAAGGGCCCTTGGCACTGGACCCCCAAGGATTACCTCATTAAGAAGCG	480	Qy	1561	ACGAGGATGTCTGGACCTTGCCCTTCAGGCGTCCCTCAGCGACTTACCTCTGTCCT	1620
Qy	481	GCACTGTTCAACTTGGCTAACGGAACTTGGAGGGCTTCCGGTCACTGGAGGCCATA	540	Db	1561	ACGAGGATGTCTGGACCTTGCCCTTCAGGCGTCCCTCAGCGACTTACCTCTGTCCT	1620
Db	481	GCACTGTTCAACTTGGCTAACGGAACTTGGAGGGCTTCCGGTCACTGGAGGCCATA	540	Qy	1621	GGAACCTCTTCAACGGCAACGTACTGGAGCCATTCAGGCTGCGCCATTCAGATGC	1680
Qy	541	ACGGCTCGGCCCTGGAGTGGCTGAGAGCTGAGCTGAGGCTGAGCTGAGGCCATA	600	Db	1621	GGAACCTCTTCAACGGCAACGTACTGGAGCCATTCAGGCTGCGCCATTCAGATGC	1680
Db	541	ACGGCTCGGCCCTGGAGTGGCTGAGAGCTGAGCTGAGGCTGAGCTGAGGCCATA	600	Qy	1681	ACGCAACAGTCTTCAAGGGCAACGTACTGGAGCCATTCAGGCTGCGCCATTCAGATGC	1740
Qy	601	AACGGGAGTTGCCCTAACAGCGTCAAGCATGGGCTGAGAGCTGAGCTGAGGCCATA	660	Db	1681	ACGCAACAGTCTTCAAGGGCAACGTACTGGAGCCATTCAGGCTGCGCCATTCAGATGC	1740
Db	601	AACGGGAGTTGCCCTAACAGCGTCAAGCATGGGCTGAGAGCTGAGCTGAGGCCATA	660	Qy	1741	AGTCGAACAGTCTTCAACTGGAAAGGCCAACCCCACAGTCCCCACAGTCGGCTGAGGCC	1800
Qy	661	CCAGCCAGGACCACTGAGTCACTTAAGGGCTTCAAGGGCTTCTTCGGC	720	Db	1741	AGTCGAACAGTCTTCAACTGGAAAGGCCAACCCCACAGTCCCCACAGTCGGCTGAGGCC	1800
Db	721	ACCACATTATCAAGTACGAGGCCATGTACCAAGGGCTTGTCCACCAA	780	Qy	1801	CITGGTGGCCCACCGTGTCACTGATGGGGCAACCTTACAGGTTGAGGGGGACCTACTTC	1860
Db	721	ACCACATTATCAAGTACGAGGCCATGTACCAAGGGCTTGTCCACCAA	780	Db	1801	CITGGTGGCCCACGGTGTCACTGATGGGGCAACCTTACAGGTTGAGGGGGACCTACTTC	1860
Qy	781	TGGAAGTCTTCCAGTGGCCCGAGATGGACAGCTCCCACTTCAAGGGCCCTTCGGC	840	Qy	1861	CCCCCTCCATGGCTCCCTGCTGGGCTCACACCGCAACTGTGCACTTCTGAC	1920
Db	781	TGGAAGTCTTCCAGTGGCCCGAGATGGCTCCCACTTCAAGGGCCCTTCGGC	840	Db	1861	CCCCCTCCATGGCTCCCTGCTGGGCTCACACCGCAACTGTGCACTTCTGAC	1920
Qy	841	ACTCCAGATGAACCGAGCCGGCTCAACTACTGCGCACGTGCTGGCCCTGGGCC	900	Qy	1921	GATCCCCATGGAAACAGCCCTCAAGGCCAGATGAGGGGAGACAGGCCCTTCCTG	1980
Db	841	ACTCCAAAGATGAAACCGAGCCGGCTCAACTACTGCGCACGTGCTGGCCCTGGGCC	900	Db	1921	GATCCCCATGGAAACAGCCCTGAAGGCCAGATGAGGGGAGACAGGCCCTTCCTG	1980
Qy	901	TGGGTGCAAAAGCATTATTAACTACCCAGAGGAGAGGGCTGGGCTCAGGGT	960	Qy	1981	AGACCAAGGTTCAATCAAGCTTCCCTGGGACATGGCTGAGGGTGTG	2040
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Qy	961	CCTCCAGATATCTGGCTTGAAGTCACTACCAACCACTGTGATAGAGGACA	1020	Qy	2041	GSTGCCTGTGACCTACCTGGACCGAGTGGACCAAGAAGCTCTCATTAACCCGGC	2100
Db	961	CCTCCAGATATCTGGCTTGAAGTCACTACCAACCACTGTGATAGAGGACA	1020	Db	2041	GSTGCCTGTGACCTACCTGGACCGAGTGGACCAAGAAGCTCTCATTAACCCGGC	2100
Qy	1021	ACGACCTCTAACGGCATCCGTTGTRACTAACAGGAACTGGCTTCAAGGGGAA	1080	Qy	2101	TGACTCAGTGGCAAGGGCACAGGTTCAAGGGTCAAGGGTCAAGGGCTCTGT	2160
Db	1021	ACGACCTCTAACGGCATCCGTTGTRACTAACAGGAACTGGCTTCAAGGGGAA	1080	Db	2101	TGACTCAGTGGCAAGGGCACAGGTTCAAGGGTCAAGGGTCAAGGGCTCTGT	2160
Qy	1081	TCACTGGAGCTGGGATGGTGTACAGCCAGCAAGGTGATGCCATTCAACAGGGAA	1140	Qy	2161	TCCGCTCTCACTGGGCTGGCTTCTGGACAGGCCACATGTGGCCGGGTGTG	2220
Db	1081	TCACTGGAGCTGGGATGGTGTACAGCCAGCAAGGTGATGCCATTCAACAGGGAA	1140	Db	2161	TCCGCTCTCACTGGGNTGGCTTCTGGACAGGCCACATGTGGCCGGGTGTG	2220
Qy	1141	TCACTCTAACGGTACTGGTACTGAGGGCAACTGGTACAGGAAAGGGTGTCAAGT	1260	Qy	2221	AATACCGGAAACGCCCTCCCGCCGGCTGCTCCGGTCAAGGGGTTCCTGGAC	2280
Db	1141	TCACTCTAACGGTACTGGTACTGAGGGCAACTGGTACAGGAAAGGGTGTCAAGT	1260	Db	2221	AATACCGGAAACGCCCTCCCGCCGGCTGCTCCGGTCAAGGGGTTCCTGGAC	2280
Qy	1201	TCCACATCTTCGCTCTCACTGGTACTGAGGGCAACTGGTACAGGAAAGGGTGT	1260	Qy	2281	CGGTTAAATTTCTGTGTTGAGTGGCTGTTACAGTGGGGTTCCTGGAC	2340
Db	1201	TCCACATCTTCGCTCTCACTGGTACTGAGGGCAACTGGTACAGGAAAGGGTGT	1260	Db	2281	CGGTTAAATTTCTGTGTTGAGTGGCTGTTACAGTGGGGTTCCTGGAC	2340
Qy	1261	TGGTCCGGGAGGGCAAGGGGGAGATGCTGAGACCACTACTACGGCTTCACT	1320	Qy	2341	GGAGGGAGGACCACTGGTACAGGAAAGGGTGTGTTGAGTGGCTGAAAT	2400
Db	1261	TGGTCCGGGAGGGCAAGGGGGAGATGCTGAGACCACTACTACGGCTTCACT	1320	Db	2341	GGAGGGAGGACCACTGGTACAGGAAAGGGTGTGTTGAGTGGCTGAAAT	2400
Qy	1321	TCCGGAGATCTGGCATGGTGAAGAAGGTGTTGAGTGGCTCATCA	1380	Qy	2401	AGTAAACAGATAATTTCGGCCACCT	2425
Db	1321	TCCGGAGATCTGGCATGGTGAAGAAGGTGTTGAGTGGCTCATCA	1380	Db	2401	AGTAAACAGATAATTTCGGCCACCT	2425
Qy	1381	CCTCTGCACTAACAGGGAACTGGGCTTGGGATCC	1440	RESULT 5			
Db	1381	CCTCTGCACTAACAGGGAACTGGGCTTGGGATCC	1440	HSDBH			
Qy	1441	TGAGGAGATGTGTCAACTACGGTCAAGGGAGACCGGACTCTGGCA	1500	LOCUS			
Db	1441	TGAGGAGATGTGTCAACTACGGTCAAGGGAGACCGGACTCTGGCA	1500	DEFINITION	Human mRNA for dopamine beta-hydroxylase	PRI 31-MAR-1995	
Qy	1501	AGACGGCTGTGGACGCCGCTTCCTGAGAAGTACTCTCCACATCAAAAGGTCAAC	1560	ACCESSION	Y00096	EC 1.14.17.1.	
Db	1501	AGACGGCTGTGGACGCCGCTTCCTGAGAAGTACTCTCCACATCAAAAGGTCAAC	1560	VERSION	Y00096..1	GI:30455	
Qy				SOURCE	Dopamine	dopamine beta-hydroxylase.	
Db				ORGANISM	Homo sapiens	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;	
						Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

QY	1561	ACGGAGGATGCTGACCTGCCCTAGGGTCCGTCTCAGGAGTCACCTCTGTTCT 1620	CDS	
Db	1568	ACGGAGGATGCTGACCTGCCCTAGGGTCCGTCTCAGGAGTCACCTCTGTTCT 1627		/note="Vector: pDNR-Dual" 1. .->112
QY	1621	GGAACTCCCTCAACGCCAACACTGTAAGCTGAAAGCCATCTCCATGC 1680		/note="Mutations: 1811:Stop->Leu" /codon_start=1 /transl_table=11
Db	1628	GGAACTCCCTCAACGCCAACACTGTAAGCTGAAAGCCATCTCCATGC 1687		/product="Homo sapiens dopamine beta-hydroxylase (dopamine beta-monooxygenase)" /protein_id="AA336138.1"
QY	1681	ACTGCCAACAGTCCTCACGCCGCGCTCCAGGGTGAACCTGAGTCAGCTGCCA 1740		/db_xref="GI: 3:0583775" /translation="MREAAFMNSTAVAFILVVALQAGSPRESPLPHIPLDPEAS LELSWAVSYTOAIIHFOLVRLRKAQVLFGMSDRBLENADLVVWTGDTAYFADAW SDOKQHLDPOQDQKQLLQVORTPEGLTLFKRPETGCPKDYLIEDGTHLTDGIL EPRPSLFANINGSGQMLQVNLQVNLQVNLQVNLQVNLQVNLQVNLQVNLQVNLQ YIKELPKGFSSHHLIKYEPITVKGNBALVHMEVOQAPMDSVPHFSGCDSXKMDK RLNYCHRVLAVALGKAFTYPEEGLAGFPGPSRYSLLEVHVNPLTEGRNDSSG SCTYNTEDERELATVGFGLIEGLVYTFWVPAIMLPRETAFLIGYCTIDCXTQALPSSCI PASQLIHTLIGRKVUVVYLVDGREVEVINDNHYSPHEFIRMLKVKVYVHPGDYLIT NNEDVCTCOPASVSQFTSUPWNNSRNDDVKAISLSPSMHCNKSSAVRFQGEWNRL PLPKVISTLEETPQOPTSQRSPAGPTVSIGSGKL."
Db	1688	ACTGCAAAGTCCTCACACTGGAAAGGCCAACACTGGTGAACCTGAGTCAGCTGCCA 1800		
QY	1741	AGTCATCCACACTGGAAAGGCCAACACTGGTGAACCTGAGTCAGCTGCCAAGGCC 1807		
Db	1748	AGTCATCCACACTGGAAAGGCCAACACTGGTGAACCTGAGTCAGCTGCCAAGGCC 1807		
QY	1801	CTGCTGGCCCCACCGTTGTCAGCATGGTGGGCAAAGGGTGAGGGGACCTACTCT 1860		
Db	1808	CTGCTGGCCCCACCGTTGTCAGCATGGTGGGCAAAGGGTGAGGGGACCTACTCT 1867		
QY	1861	CCCCCTCTCCATGCTGCCCTGGGCTCACACCGGCACTGTGCACTACTCTGCGAC 1920		
Db	1868	CCCCCTCTCCATGCTGCCCTGGGCTCACACCGGCACTGTGCACTACTCTGCGAC 1927		
Qy	1921	GATCCCCATGGAACAGCCCTGACGCC 1948		Query Match Best Local Similarity 66.2%; Score 1805.2; Matches 1807; Conservative 99.8%; Pred. No. 0; MisMatches 0; Indels 0; Gaps 0;
Db	1928	GATCCCCAAGGACAGCCCTGACGCC 1955		
Qy	1921	GATCCCCATGGAACAGCCCTGACGCC 1948		
Db	1928	GATCCCCAAGGACAGCCCTGACGCC 1955		
RESULT	6			
BT007470				
LOCUS				
DEFINITION		Synthetic construct Homo sapiens dopamine beta-hydroxylase		
ACCESSION				
VERSION				
KEYWORDS				
SOURCE				
ORGANISM				
REFERENCE				
AUTHORS				
KEYWORDS				
TITLE				
JOURNAL				
REFERENCE				
AUTHORS				
KEYWORDS				
TITLE				
JOURNAL				
COMMENT		This CDS clone is a part of a collection of human full length expression clones generated by BD Biosciences Clontech and the Harvard Institute of Proteomics. Each CDS has been cloned in two forms: with and without stop-codon (to allow fusion with C-terminal tag). The CDS has been directionally cloned using BD In-Fusion™ cloning system between the SalI and HindIII sites of the pDNR-DUAL vector. Additional sequences in the clone: 'ACC' after SalI site and before 'ATG' to provide Kozak consensus sequence; 'GG' after last codon and before HindIII site to maintain reading frame.		
FEATURES				
source				
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				/organism="synthetic construct"
				/mol_type="mRNA"
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				/clones="GH010591.0"
				/clone_lib="BD Creator (TM) CDS Library derived from MGC collection"
				/lab_host="DH5alpha T1 resistant"
QY	693	AAGGAGGCTCCAAGGGCTTCCTCGGCCACCATATTACAACTACGGCCCATCTGTAC 752		

Db	133	GCATCCCCCTGGGACCCCGAGGGGAACTCTGGAAATGTGAGG	192
Qy	199	AGGCCATCATTCAGGCTCAGGCTCCAGGCTGGGACTCAAGG	258
Db	193	AGCCATCATTCAGGCTCAGGCTCCAGGCTGGGACTCAAGG	252
Qy	259	CGAACCGGGAGCTTGAAGACGAGATCTCGTGGCTGGGACACTG	318
Db	253	CGAACCGGGAGCTTGAAGACGAGATCTCGTGGCTGGGACACTG	312
Qy	319	CCTATTGCGGAGCGCTGGAGTGAAGGGGAGAATCCTGGATGG	378
Db	313	CCTATTGCGGAGCGCTGGAGTGAAGGGGAGAATCCTGGATGG	372
Qy	379	ACTACCAGCTGTGAGGGTGGAGGACCCAGGGCTGACAGAGC	438
Db	373	ATTACCAGCTGTGAGGGTGGAGGACCCAGGGCTGACAGAGC	432
Qy	439	CCTTNGGACCTTGACCCAGGATTACCTCATTTGAAGAACGGG	498
Db	433	CCTTNGGACCTTGACCCAGGATTACCTCATTTGAAGAACGGG	492
Qy	499	ACGGATCCTGGAGGAGCCTGGCTACTGGGCGCTGAGA	558
Db	493	ACGGATCCTGGAGGAGCCTGGCTACTGGGCGCTGAGA	552
Qy	559	TGGGGCTGAGGGTGCACCTCTCTGAGGGCCATATGCCCTCAG	618
Db	553	TGGGGCTGAGGGTGCACCTCTCTGAGGGCCATATGCCCTCAG	612
Qy	619	ACGGCTGACCCATGGGGAACTCTCCGAAACTCCGAAAGCCT	678
Db	613	ACAGTCGACCCATGGGGAACTCTCCGAAACTCCGAAAGCCT	672
Qy	679	ACGTGTGTACATTAAGGGCTTCCAAAGGGTTCTCTGGACCA	738
Db	673	ATTGGTGTACATTAAGGGCTTCCAAAGGGTTCTCTGGACCA	732
Qy	739	AGGCCATCTCCACCAAGGGCTTCCACATGGGACTCTCCAG	798
Db	733	AGGCCATCTCCACCAAGGGCTTCCACATGGGACTCTCCAG	792
Qy	799	CCCCGAGATGGAGCAGCTCCCACTTCAAGTGAACCCG	858
Db	793	CCCCGAGATGGAGCAGCTCCCACTTCAAGTGAACCCG	852
Qy	859	ACGGCTTAACTAACACTGGCCACAGTGTGGCCCTGGGACTT	918
Db	853	ACGGCTTAACTAACACTGGCCACAGTGTGGCCCTGGGACTT	912
Qy	919	ACTACCCAGGAAAGGGCCCTTGGCTCAAGGGGATCTGGG	978
Db	913	ACTACCCAGGAAAGGGCCCTTGGCTCAAGGGGATCTGGG	972
Qy	979	TGGAAACTTCACTACCAACCCAGCTGGTGAAGGGCATTT	1038
Db	973	TGGAACTTCACTACCAACCCAGCTGGTGAAGGGCATTT	1032
Qy	1039	GCTTGACTACACAGGCAAGTGGCCAGCTGGGACTCTGGG	1098
Db	1033	GCTTGACTACACAGGCAAGTGGCCAGCTGGGACTCTGGG	1092
Qy	1099	TGTACAGGCAAGTGGGACTCTGGGACTCTGGGACTCTGGG	1158
Db	1093	TGTACAGGCAAGTGGGACTCTGGGACTCTGGGACTCTGGG	1152
Qy	1159	GCACGCCAAACTGACCCAGCTGGGACTCTGGGACTCTGGG	1218
Db	1153	GCACGCCAAACTGACCCAGCTGGGACTCTGGGACTCTGGG	1212
Qy	1219	AGCTCCACACACACTGACTGGGAAAGGTGGTCAAGTGT	1278
Db	1213	AGCTCCACACACACTGACTGGGAAAGGTGGTCAAGTGT	1272

ESINTSGIHTGJQVRQLIKPSIPKPALLADTRMEIRADFLVLPQQTYWCVTEFL DGFPKRHIIWMEPVIVTVEPQACAEFETTGCDSKPIKPKORIINFCE HVLAALWAGAKAFYYPPEAGLAFCGGCTCGGGAAATTGCTCCACTGCAGGTAAATAGATA AALRPFADIGMELGLATTTAGAACGTCGCTGGAAATTGCTCCACTGCAGGTAAATAGATA THLTGRKVVTLLARDGRETEIVNRDNHNSPHFOBIRMKKVSQVPLVYCTDQLALPASCHIIFASQLL EDRQASVPEQFASVPNNSPNREVVKALYGFAPISMHCNRSSAVRLEGWNRQPLPEII SRLEBPTPHCPASQAQSAPGPTVLNISGGKG"	
2333 AGGGTATTAGCTAGTTAGAGCTAGCCTGGGAATTGCTCCATTCTCTGAGTAACAGATA 2412 2332 AGCCACTTAGCTAGCTAGTTAGAGCTAGCCTGGGAATTGCTCCACTGCAGGTAAATAGATA 2391	
2413 TTTTGCCCACTTAAGGGAAAGCCTGAGAACACTATACCA-----AAAGAGCAGGG 2467 2392 TTTCGCCCACTTAAGGGAAAGCCTGAGAACACTATACCA-----AAAGAGCAGGG 2450	
2468 GCAAAGATTCAGCGGGCTTCGGCGGGGTTCACTGGGGATTAATTAGCACCA 2527 2451 GCGAAGATTCAGCAAGGATCCCGGGTCAAGCTGGGATGGGGAT-TAGCCA 2509	
2328 GCTTGCTCTTCGCGGCTTCAGCTGGGGTCAAGCAGAC-----GGGTGGAGTCAGGG 2581 2510 GGTGCTCTTCACGTTGAGGGTCAACGTCGCTGGGTCAAC 2569	
2582 CTTGTGCTTCGCGGCTTCAGCTGGGGTCACTGGGAGCTTCACT 2641 2370 CTGTCAGAAGCCGGGTCATCTGGGCTGGGTCACTGGGCGGGCAATTCACT 2629	
2642 TCTGTACCTCACTTTCTCATCTGTAAAACCGGGCTATGCCGTCGGGCTTAATGACC 2701 2630 CCCTCACCTGGTTTCTCATCTGTAAAATGGCCAACGCTGTGTTGATGAGAT 2689	
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Bos taurus	
Organism	
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1. (bases 1 to 2317)	
Wu, H.J., Farmer, R.J., Koop, A.H., Rozansky, D.J. and O'Connor, D.T. Molecular cloning, structure, and expression of dopamine-beta-hydroxylase from bovine adrenal medulla J. Neurochem. 55 (1), 97-105 (1990)	
90285664	
PUBMED 1693949	
REFERENCE 2 (bases 1 to 2317)	
AUTHORS Wu, H.J., Farmer, R.J., Koop, A.H., Rozansky, D.J. and O'Connor, D.T. TITLE Direct Submission JOURNAL Submitted (07-JAN-1999) Medicine (911H), UCSD, 3350 La Jolla Village Drive, San Diego, CA 92161, USA Location/Qualifiers 1..2317 1. "2317 1. "2317 1. "2317	
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DEFINITION Genomic sequence from Human 9q34, complete sequence.

ACCESSION AC000404_1 GI:2133957

VERSION HTG.

KEYWORDS Homo sapiens (human)

ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 46651)

AUTHORS Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W., Pasman,K.H. and Lander,E.S.

TITLE Genomic sequence from Human 9q34

JOURNAL Unpublished

REPEAT_REGION (bases 1 to 46651)

AUTHORS Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W., Pasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barns,N., Brown,K., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J., Gage,D., Geraigery,K., Hagos,B., Jacobot,L., Lane,M., Mackenzie,J., Marquis,N., McDermit,J., Moloney,N., Morrow,J., Nachman,A., Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J., Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and Zody,M.

Direct Submission

Submitted (08-APR-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 3 (bases 1 to 46651)

AUTHORS Hawkins,T.L., Reeve,M.P., Christoffersen,A., Birren,B.W., Pasman,K.H., Lander,E.S., McKernan,K., Munro,C., Richardson,P., Barns,N., Chang,A., Cooke,P., Daly,M.J., Forrest,C., Fripp,W.J., Gage,D., Geraigery,K., Hagos,B., Jacobot,L., Lane,M., Mackenzie,J., Marquis,N., McDermit,J., Moloney,N., Morrow,J., Nachman,A., Naylor,J., O'Connor,T., Peterson,K., Rollins,G., Spencer,J., Stilwell,J., Stone,C., Strickland,C., Sydney,K., Wilmer,F. and Zody,M.

Direct Submission

Submitted (29-MAY-1997) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On May 29, 1997 this sequence version replaced gi:1929451. The Staden databases, finishing information, and all chromatographic files used in the assembly of this clone are available from our anonymous ftp site.

All repeats were identified using RepeatMasker: Smit, A.F.A. & Green, P. (1996-1997) <http://ftp.genome.washington.edu/RM/RepeatMasker.html>.

FEATURES source

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REFERENCE	1 ('bases 1 to 2037)			
AUTHORS	Kobayashi,K., Kurokawa,Y., Fujita,K. and Nagatsu,T.			
TITLE	Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation			
JOURNAL	Nucleic Acids Res. 17 (3). 1089-1102 (1989)			

QY	121	AGAGCCCCCTCCCTATACATCCCCCTGAGACCCGGAGGGTCCCTGGAGCTCATGGA	180	Qy	840	GACTCACAGATGAAACCCGAGCCGCCCACTACTGCCGCCACTGCGCTGCAGCTGGGCC	899
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REFERENCE				RESULT 22			
AUTHORS	Ernsberger U., Reissmann E., Mason J. and Rohrer H.			HSDBH3			
TITLE	The expression of dopamine beta-hydroxylase, tyrosine hydroxylase, and Phox2 transcription factors in sympathetic neurons: evidence for common regulation during noradrenergic induction and diverging regulation later in development			LOCUS	Human DNA for dopamine beta-hydroxylase exon 3	PRI 04-MAY-1990	
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Institut f. Anatomie und Zellbiologie III, Im Neuheimer Feld 307, D-69120 Heidelberg, GERMANY				ORGANISM		Eukaryota; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo sapiens	
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Qy	475 AAGACGGCACTGTCCACTTGTCTAAGGGATCCCTGGAGGCCCTTCGGGTCACGGAGG 534	Qy	899 CCTGGGTGCCAAGGCATTACTACCAAGGGAGGCCCTTCGGGGTCACGGAGG 958
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		ACCESSION	DMTBHMR
		VERSION	270316
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		SOURCE	Drosophila melanogaster (fruit fly)
		ORGANISM	Drosophila melanogaster
			Bukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriidae; Drosophilidae; Drosophila.
		REFERENCE	1 (bases 1 to 2894)
		AUTHORS	Monastirioti M., Lian C. B. Jr. and White K.
		TITLE	Characterization of Drosophila tyramine beta-hydroxylase gene and isolation of mutant flies lacking octopamine
		JOURNAL	J. Neurosci. 16 (12), 3900-3911 (1996)
		MEDLINE	9624206
		PUBMED	8656284
		REFERENCE	2 (bases 1 to 2894)
		AUTHORS	Monastirioti M.
		TITLE	Direct Submission
		JOURNAL	Submitted (29-MAR-1996) Maria Monastirioti, Insect Molecular Genetics Group, IMBB, Foundation for Research and Technology, Hellas, Vasilika Voutou, Heraklion, Crete, 71110, Greece
		FEATURES	Location/Qualifiers
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			/db_xref="PDB:10010329"
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			EDHQPAFLPNVTAPEHEAVKMLQLRLADKPLIPSELDLIPAPISQETWYCH
			VQLRBEMLNRKKHIVQEPLRTVHMEVFKEAGEHBSBPLYNGDCEQLPRAK
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			KMSKRCIVSIASTAVMELGLEYTDKMDAPPQTAFPLSSYCVADCTRAALPATGTLFEGQ
			LHTHJRGVRVSLTRHPRGEQEIRVNRDDYSNHFQMRITLQYKPRVLPGDALVTFCY
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BASE COUNT	52 a 83 c	52 a 83 c	78 g 49 t
ORIGIN			
Query Match	8.8%	Score 239.6;	DB 9;
Best Local Similarity	94.7%	Pred. No. 1..9e-34;	Length 262;
Matches 248; Conservative	0;	Mismatches 14;	Indels 0;
		Gaps 0;	Gaps 0;
Qy	839 CGACTCCAAAGATGAAACCGACGCCCTCAACTGCGCCACGTGCTGGCTGGC 898		
Db	1 CGACTCCAAAGATGAAACCTGACGCCCTCAACTGCGCCACGTGCTGGCTGGC 60		

BASE COUNT	707	a	752	c	730	g	705	t
ORIGIN								
Qy	VLHNGARSSNVRSLIEWTQPRTDQLTYMMQDPLSMOONRSDFGTRFEGRSSMEVGAAAT							
Db	VQIRIPHRKLCPNPYNNPLWKPLEKDCDLIGEICY"							
Query Match	8.4%		Score 228.4 ; DB 3 ;	Length 2894 ;				
Best Local Similarity	53.5%		Pred. No. 1..6e-32;					
Matches	594;		Mismatches 501; Indels 15;			Gaps 5;		
Qy	629 CATGGAGTCAGCTCCAAATTATCCAGATCCCCAGGCCAGGACACAGCTTGTTGCTA							
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Qy	689 CATTAAAGGAGTTCAAAAGGGCTTCTCGGCACCACTATTACAAGTACAGGCCAACATCGT							
Db	1041 CGTTAGCAGACTGG-- -AGGGAAATTCGGGCTGCCTCATCGTGTGAGCC							
Qy	749 CACCAAGGGCATATGGGCCCTTCTCACCAATGGAGTCTCCAGTGGCCGGGAGAT							
Db	1098 GCTTATTCGAAAGCGCCGATCGTGGATCATCGAGGTGTTCACTGGAGCTGGTGA							
Qy	809 GGACAGGGTCCCCACCTAGGGGGCTGGACTCCAAGTGAACCCGCGCTCAA							
Db	1158 GCACGGGAGATTCCCTGTATA--CGGGCACTTGAAAGAGTTGCAACGGGAA							
Qy	869 CTACTCCGGCACGPTCTGGCCGCTGGCCCTGGCTGCCAGGCAATTACTACCCAGA							
Db	1215 GATCTCTCAAAGTATGGCTCTGTGGCCATGGGCTGCACCTTACCTATCC							
Qy	929 GGAAGGGCCCTTGCCTTGGGGTCTGGGTCAAGATATCTGGCTGAAAGTCA							
Db	1275 GGAAGCGGTCTACCAATCGGGACCCGGCTCAATCCGTAACGTGGTGTACA							
Qy	989 CTACCAAAACCACTGGTATAGAAAGAGAAACGACTCTAGGCATCCGCTTGTACTA							
Db	1335 TTTCATTTAATGGCAAGCTGGGCTTGGTGGAACTCCGGTTTCGAT-							
Qy	1049 CACGCCAAGGTGGCGCTCAACCGGGGATCATGGAGGTGGACTGGTACAGGCC							
Db	1392 GATGTAAGGACTGGTCACTATGGGGCTTATGGAATCTGGCTGACTACCGGA							
Qy	1109 AGTGTGGCCATTCCACCGGAGCCGGCTTCACTCTCATGGTACTGGCTACAGGACAA							
Db	1452 CAAATGGCCATTCCCTGGCCAACCCGATTCGGCTGAGGGTATTGTGGCGGA							
Qy	1169 GTGCAACCGAGGGCACTGGCTCCCTGGGATCCACATCTGGCTCTGACTCACAC							
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Db	1572 GCATGCTGGGTGTCCTACCCGACACTTTCGGGAGGCTGGCGGA							
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Db	1632 GGTAACCGGGATGACTCACTGGCAATCTCCGAGATGCGACCCCTGCACTACAA							
Qy	1349 CGTGTGTCATGGAGATGTTCACTACCCCTGAGCTGAAACGGGAGACCG							
Db	1692 GCGCGCTGCTGGGGCACGGCTTGGTAACTACCTGACTACACAAAGG							
Qy	1409 GGAGCTGGCCAGAGCACGCTGGGGCTTCTGGGATCTGGGAGATGTTGCTCAACTGTGCA							
Db	1749 TGCAAGACGGCTCAGGGATCTCCATAGCTGGTGTGCTAACATATCCA							
Qy	1469 CTACTACCCAGACAGCACGCTGGGGCTTCTGGGACTCTGGGAGCTGGCTGCA							
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Qy	1529 GAAGTACTCCACCTCATACAGETTAACAAACGGATGCTCACCTGGCTCAGGG							
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DEFINITION	RESULT 29	C126203	AC126203	225079 bp DNA linear HTG 15-NOV-2002
AUTHORS	OCUS	Rattus norvegicus clone CH230-177E3, WORKING DRAFT SEQUENCE, 2 unorderd pieces.	AC126203	HTGS PHASE1; HTGS_DRAFT; HTGS_FULLTOP.
VERSION	REVISION	AC126203.3	GI:25007867	Rattus norvegicus (Norway rat)
SOURCE	ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eurelostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.	1 (bases 1 to 225079)	Muzny, D., Marie, Metzger, M., Lee, Abramzon, S., Adams, C., Alder, J., Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D., Anyalebechi, V., Bao, Y., Bao, Y., Bao, Y., Bao, Y., Bao, Y., Bao, Y., Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F., Biswalo, K., Blair, J., Blankenburg, K., Bluyt, P., Brown, M., Bryant, N.N., Buhay, C., Burch, P.P., Burrell, K., Calderon, B., Cardenas, V., Carrer, K., Cavaros, I., Ceasar, H., Center, A., Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J., Cleveland, C., Cockrell, R., Cox, J.C., Coyle, M., Cree, A., D'Souza, L., Davila, M.L., Davis, C., Davy-Carroll, L., De Andra, C., Dederich, D., Delgado, O., Denson, S., Deramo, C., Ding, Y., Dinh, H., Diryaya, K., Draper, H., Dugan-Rocha, S., Dunn, A., Durbin, K., Duval, B., Eaves, K., Egan, A., Escotto, M., Eugene, C., Evans, C.A., Failes, T., Fan, G., Fernandez-S, Pinley, M., Flagg, N., Forbes, L., Foster, M., Foster, P., Fraser, C.M., Gabisi, A., Garcia, R., Garcia, A., Garner, T., Garza, M., Gregorio, E., Geer, K., Gill, R., Gray, M., Guerra, W., Guerevara, W., Gunaree, P., Haaland, W., Hamil, C., Hamilton, C., Harvey, Y., Havlik, P., Hawes, A., Henderson, N., Hernandes, J., Hernandes, R., Hines, S., Hladun, S.L., Hodges, M., Hollins, B., Howells, S., Hulluk, S., Hume, J., Idlebird, D., Jackson, A., Jackson, L., Jacob, L., Jiang, H., Johnson, B., Johnson, R., Olivet, A., Karwowski, S., Kelly, S., Kelly, S., Khan, Z., King, L., Kovar, C., Kraft, C., Kraft, C.L., Lebow, H., Levan, J., Lewis, J., Li, Z., Liu, J., Liu, J., Liu, W., Liu, Y., London, P., Longacre, S., Lopez, J., Loreshewara, L., Loulides, H., Lozano, R.J., Lu, X., Ma, J., Mahendartne, M., Mahmoud, M., Malloy, K., Mangum, A., Mangum, B., Mapus, P., Martin, K., Martin, R., Martinez, E., Mawhinney, S., McLeod, M.P., McNeill, T.Z., Meenen, E., Milosavljevic, A., Miner, G., Marin, E., Montemayor, J., Moore, S., Morgan, M., Morris, K., Morris, S., Munidasa, M., Murphy, M., Nair, L.,

FEATURES	*	223773	223872;	gap of unknown length		Qy	61	CAGCAGTGGCCATCTTGGTATCCCTGGAGGACTGGCCCGTGGCTCCCGTG	120
source		223873	225079;	Contig of 1207 bp in length.		Db	278	CAACATAACCATCTCCATAATCCCTAAATAACCGACTAACAACTGACTCCCGTA	219
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	Best Local Similarity	81.0%	Pred. No. 2	8e-31;					
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Qy	15	AGCTGCCGCCAGATGGGGAGGGAGCCTTCATGATCACAGCACAGCAGTCATGC	74						
Db	165644	AGCTCCCAAGCCCCAGGTCCGGTCAAGTGGACTGGCATGATGACTGGCATC	165703						
Qy	75	TTCCTGGTCACTCTGGTGGCCGACTGGGGTTGCTGGTGGAGGCCCTCCGCC	134						
Db	165704	TTCCTGGTCACTCTGGTGGCCGACTGGGGTTGCTGGTGGAGGCCCTCCGCC	165763						
Qy	135	TATCACATCCCCTGGACCAGGGTCCCTGGAGTCATGGATGAGTACACC	194						
Db	165764	TACACATCCCCTGGACCTGGAGGACTTGTAGGTCTGTGGAACTGATGATGAC	165823						
Qy	195	CAGGAGGCCATCATTCAGTCAGTCCCTGGCGAGGGTCANGCTGGCTCTGG	254						
Db	165824	CAGGAGATCATCACTTCAGTCAGTCCCTGGCGAGGGTCANGCTGGCTCTGG	165883						
Qy	255	ATGTCACCTGGAGCTTGAGAAGATCTGGTGGCTCTGGACGGATGGGAC	314						
Db	165884	ATGTCGCACTGGAGTGAGATGGAGAACGCAACTCTGGTCACTGGAC	165943						
Qy	315	ACTGCCATTGGGG 330							
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RESULT	30								
LOCUS	AM347199		2037	bp	DNA	linear	PAT 01-FEB-2002		
DEFINITION									
ACCESSION	AM347199								
VERSION	AM347199								
KEYWORDS	.								
SOURCE									
ORGANISM									
REFERENCE									
AUTHORS	Olek,A.; Piepenbrock,C. and Berlin,K.								
TITLE	Diagnosis of diseases associated with the immune system								
JOURNAL	Patent: WO 020028-A 2270 03-JAN-2002;								
FEATURES									
source	1.	.2037							
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BASE COUNT	417	a	49	c	558	g	1013	t	ORIGIN
ORIGIN									
	Query Match	7.1%	Score 193;	DB 6;	Length 2037;				
	Best Local Similarity	74.2%	Pred. No. 6.	7e-26;					
	Matches	244;	Conservative 0;	Mismatches 85;	Indels 0;	Gaps 0;			
Qy	1	TGAGTCGCTGGCCATCTGGTGGCTCTGGGAGGCGCCATGCTGGCTCC	60						
Db	338	CAACAAATACCATCTTCATAATCCCTAAACTCTAACATACATACACA	279						
Qy	61	CAGCAGTGGCCATCTGGTGGCTCTGGGAGGCGCCATGCTGGCTCC	60						
Db	278	CAACAAATACCATCTTCATAATCCCTAAACTCTAACATACATACACA	279						
Qy	121	AGAGCCCTCCCTCCATACATCCCTGGGAGGCGCCATGCTGGCTCC	60						
Db	218	AAACACCCCTCCCTATACATCCCTGGGAGGCGCCATGCTGGCTCC	240						
Qy	181	ATGTCAGCTACCCAGAGCCATCTGGTGGCTCC	60						
Db	158	ATATCAACATACCCAAACCATCTTCATAACAAATCTCAAACATA	279						
Qy	241	GGCTCTGGTGGAGTCGGCCAGCTGGCTGGAGCTGAGCTGAGCTCT	60						
Db	98	ACGTCTTATTAAATCCGACCTAACATCAAACCTCTGAATACTCT	39						
Qy	301	GGACCCAATGGGACACTGCCATTGTCGG 329	60						
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BASE COUNT 759 a 657 c 630 g 750 t

ORIGIN

Query Match	Score	Length	DB	Pred.	No.	Mismatches	Indels	Gaps	;
Best Local Similarity	6.3%	2796							
Matches	620;								
Conservative	48.1%;								
	0;								
Qy	282	GCAGATCTCTGGCTCTCGACCAGATGGGACACTGGCTATTTGGAGCAGCTGGAGT 341							
Db	2	GCAGACATCTGGTAGGGAGTGCCCGGGCCCTACCTCCAGAACATTCAAC 61							
Qy	342	GACCGAAAGGGCAGATCACCTGATTCGCCAGGAACTTCAAGGGCTTTCAGACCTGGAGT 401							
Db	62	AACCGAGAACAGAGCTGGAAAGATGCCAGGAGATTAACCACTGATTCAGAT 121							
Qy	402	AGGACCCAGAAGGCCCTGACCCCTGTTTCAGAGGCCCTTGGCACCTGGACCCCCAG 461							
Db	122	GAGAACGACACAGACAGATGGAGACCTGCCCACCTGGTCAACGGGACTCTGGATGCCAAAT 181							
Qy	462	GATTACCTATTGAGACGCCACTGCCACCTGGTCAACGGGACTCTGGATGCCAAAT 521							
Db	182	GACAGAGCTTCAGGATGACCGATGACCGTGAAGGTATCTGGCCCTAACCATGAGATCCCAC 241							
Qy	522	CGGTCACTGGGGCATCACGGCTGGCTGAGATGGGGCATGGGGTGCAAGGGTGCACTGGCT 581							
Db	242	GGAGAAATCGTGTCC--GAGTACCATGCTTAATAGGGCAAGGGTGTCAAGGT 298							
Qy	582	CTGAAGCCCAAATATCCCCAACCGGAGTGCCTCTAGAAGGGTGCACCATGGGGTCCA 641							
Db	299	CTGATCTGAGAAGCCA--TGTGGTGTCACTGTACTTGTATCTGGTCTGTT 355							
Qy	642	GCTCCCAATATCCGAGATCCCGAGCTGGCTGCTACATTAGGAGT 701							
Db	356	AATCRAAAAGTCCATTCAAGAAAATCATGTTGATAAAAGTGGGCCAAATAGTTAAGAT 415							
Qy	702	CCADAGGGCTCTCGGACCAATTATCAAGTACGACCCCATGTCAGCTGGCT 761							
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Qy	762	GAGGCCCTTGTCCACCATGGAAAGTCACTGGCTGCCCCGA---GATGGACAGGCT 818							
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gene	596	ACTGTGATTCCTCGCTGGGGATTTGGTGGAGGGCTTACCTATCCACTCGTGGC 655							
	939	CTTGCTCTGGGGTCCAGGTCTCCAGATATCTCCGCTGGAAAGTCACTACACAC 998							
	656	TTATCCCTGGCATGGATCCTGGTCACTGAGTCAATACTGCTTTAGGTCACTA 715							
	999	CCACTGGTATAGAGGAGAAAGCACTCTCAGCATCGCTGTACTACAGGCCAG 1058							
	716	CCCGCACGGAGGAGGGCTTAATAGACAGTTTCGGGTGAGGGTTTCATCATCA 775							
	1059	CTGCGCGCTCAAGGCGGGATCATGGAGTCACTGTGTAACCGCAGTGTGGATGCC 1118							
	776	ATAAGGAGATATGGCAGGAGTCACTGTGTAACCGCAGTGTGGATGCCAGTCA 835							
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	1196	TATTACCAAGAGTTAACCTGACGGGTCTCCAGATCCCAAGACATCATGGACAGTGTG 1255							
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	LOCUS								
	DEFINITION								
	X13262								
	VERSION	X13262..1							
	KEYWORD	GI:30467							
	ORGANISM	alternative splicing; dopamine beta-hydroxylase; hydroxylase.							
	SOURCE	Homo sapiens (human)							
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarhinini; Hominidae; Homo.								
	REFERENCE	1 (bases 1 to 185)							
	AUTHORS	Kobayashi, K., Kurisawa, Y., Fujita, K. and Nagatsu, T.							
	TITLE	Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation							
	JOURNAL	Nucleic Acids Res. 17 (3), 1089-1102 (1989)							
	MEDLINE	8916241							
	PUBLISHED	292261							
	REFERENCE	2 (bases 1 to 185)							
	AUTHORS	Nagatsu, T.							
	TITLE	Direct Submission							

JOURNAL	Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT	Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
FEATURES	Location/Qualifiers
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intron	BASE COUNT
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Qy	1013 AGGACAAACGACTCCCTCAAGCATCGCTTACTACAGCCAAAGCTGGGCCCTTCAA 1072 8 AGGAAGAAGACTCTAGACATGGGACTGTGTTACTACAGCCAAAGCTGGGCCCTTCAA 67
Db	1073 CGGGGGATCATGGAGCTGGGACTGTGTTACGGCAATGGCATTACACGGGA 1132 68 CGGGGGATATGGCTGGGACTGTGTTACGGCAATGGCATTACACGGGA 127
Qy	1133 GACCCGCTTATCTCTACGCTGCTACTGACAGTGACAGTGACCTGG 1182 Db 128 GACGCCCTTCATCTCACGCTACTGACAGTGACCTGG 177
RESULT 39	
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DEFINITION	Human sapiens clone BPR-4 mRNA sequence.
ORGANISM	Homo sapiens
ACCESSION	2906 bp
KEYWORDS	GI:4928110
SOURCE	Homo sapiens (human)
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE	1 (bases 1 to 2906)
AUTHORS	Gilbert,J.R., Kumar,A., Newey,S., Rao,N., Ioannou,P., Qiu,H., Lin,D., Xu,P., Pettenati,M.J. and Pericak-Vance,M.A.
TITLE	Physical and cDNA mapping in the DBH region of human chromosome 9q34
JOURNAL	Hum. Hered.
MEDLINE	50 (3), 151-157 (2000)
PUBMED	10686491
REFERENCE	2 (bases 1 to 2906)
AUTHORS	Gilbert,J.R., Kumar,A., Newey,S. and Pericak-Vance,M.A.
TITLE	Direct Submission
JOURNAL	Submitted (18-FEB-1999) Center for Human Genetics, Duke University Medical Center, Research Park 2, DUMC, Durham, NC 27710, USA
FEATURES	Location/Qualifiers
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intron	BASE COUNT
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Db	1572 TGACCTGCCCCTGAGGTACCTCTGGAACTCTTCAGGTTACCTCTGGAACTCTTC 1631 403 TGCACCTGCCCCTGAGGTACCTCTGGAACTCTTCAGGTTACCTCTGGAACTCTTC 344
Qy	1632 AACCGGAGCTACTGAAGGCCCTGTACAGCTTCGGCCATTCATGCACTGAAACAG 1691 343 AACCGGAGCTACTGAAGGCCCTGTACAGCTTCGGCCATTCATGCACTGAAACAG 284
RESULT 40	
Db	HSDBH1 HSDBH1 HSDBH1 HSDBH1
DEFINITION	Human DNA for dopamine beta-hydroxylase exon 11 (EC 1.14.17.1).
ACCESSION	X13267
VERSION	X13267.1 GI:30461
KEYWORDS	alternative splicing; dopamine beta-hydroxylase; hydroxylase.
SOURCE	Homo sapiens (human)
ORGANISM	Homo sapiens
REFERENCE	Kobayashi,K., Kurosa, Y., Fujita, K. and Nagatsu, T.
AUTHORS	1 (bases 1 to 178)
TITLE	Human dopamine beta-hydroxylase gene: two mRNA types having different 3'-terminal regions are produced through alternative polyadenylation
JOURNAL	Nucleic Acids Res. 17 (3), 1089-1102 (1989)
MEDLINE	89160241
PUBMED	2922261
REFERENCE	2 (bases 1 to 178)
AUTHORS	Nagatsu, T.
TITLE	Direct Submission
JOURNAL	Submitted (14-OCT-1988) Nagatsu T., Department of Biochemistry, Nagoya University, School of Medicine, Nagoya 466, Japan
COMMENT	Map data from Craig et al. Cytogenet. Cell Genet. 48:48-50 (1988).
FEATURES	Location/Qualifiers
source	1..178
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intron	intron
mRNA	intron
intron	intron
BASE COUNT	32 a 68 c 39 g 39 t
ORIGIN	Query Match Score 6.0%; Best Local Similarity 98.8%; Matches 165; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
Qy	1547 CAACAGGTTCAACAAACAGGAGTCTGACCTCTGCCCTAGGCTCCCTAGGAGTCTAGGAGT 1606 4 CACCGGTTCAACAAACAGGAGTCTGACCTCTGCCCTAGGCTCCCTAGGAGTCTAGGAGT 63
Db	1607 CACCTCTGTTCTCTGGAACTCTTCACCGCAGTACTGAAGGCCCTGTACAGCTTCGC 1666 64 CACCTCTGTTCTCTGGAACTCTTCACCGCAGTACTGAAGGCCCTGTACAGCTTCGC 1222
BASE COUNT	918 c 862 g
ORIGIN	

Qy 1667 GCCCATCTCCATGCAACTGCAACAAAGTCCTCAGCCGTCCGGTTCCAGG 1713
Db 124 GCCCATCTCCATGCAACTGCAACAAAGTCCTCAGCCGTCCGGTTCCAGG 170

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Job time : 9709 secs

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